

SEQUENCE LISTING

<110> RONSIN, CHRISTOPHE
SCOTT, VERONIQUE
TRIEBEL, FREDERIC

<120> PEPTIDE COMPOUND DERIVED FROM A SHIFTED ORF OF THE ICE
GENE

<130> 065691-0263

<140> 10/019,219

<141> 2001-12-28

<150> PCT/FR00/01791

<151> 2000-06-27

<150> FR 99/08224

<151> 1999-06-28

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 162

<212> PRT

<213> Homo sapiens

<400> 1

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Cys	Trp	Leu	Pro	Trp	Arg	Thr	Trp	Trp	Trp	Ser	Ser	Ser	Ser	Thr	Ala
			20				25						30		

Trp	Val	Ser	Trp	Ala	Ser	Ser	Ala	Leu	Glu	Thr	Ser	Thr	Gln	Pro	Ala
	35						40					45			

Thr	Gly	Ala	Thr	Trp	Thr	Lys	Trp	Leu	His	Tyr	Ala	Gly	Ser	Ser	Arg
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Ile	Ser	Pro	Thr	Leu	Glu	Ala	Thr	Leu	Thr	Val	Ser	Pro	Phe	Leu	Ala
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Ser	Leu	Arg	Val	Ala	Arg	Val	Cys	Leu	Arg	Leu	Leu	Cys	Pro	Pro	Tyr
			85						90					95	

Pro	Lys	Asp	Ser	Ser	Thr	Glu	Pro	Ser	Trp	Arg	Val	Ala	Trp	Pro	Ser
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Cys	Pro	Ala	Ser	Leu	Pro	Ala	Gln	Leu	Met	Ser	Ser	Pro	Arg	Trp	Trp
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Pro	Thr	Cys	Leu	Pro	Val	Thr	Lys	Leu	Thr	Leu	Arg	Pro	Trp	Trp	Ala
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Ala Cys Gly Ala Arg Val Lys Arg Arg Phe Leu Gln Leu Thr Ser Leu
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Ser Arg

<210> 2
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 ctggagacaa gcacgcaacc ggcaactggg gctacctgga ccaagtggct gcactacgct 180
 ggggtccagca gaatatcgcc cactttggag gcaaccctga ccgtgtcacc atttttggcg 240
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 ctgatgtcat ctccacgggtg gtggccaacc tgtctgcctg tgaccaagtt gactctgagg 420
 ccctggtggg ctgcctgcgg ggcaagagta aagaggagat tcttgcaatt aacaagcctt 480
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 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: Primer

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ctt ctg ctg ctt ctt gtc cgg ggc cag ggc cag gac tca gcc agt ccc 96
 Leu Leu Leu Leu Leu Val Arg Gly Gln Gly Gln Asp Ser Ala Ser Pro
 20 25 30

atc cgg acc aca cac acg ggg cag gtg ctg ggg agt ctt gtc cat gtg 144
 Ile Arg Thr Thr His Thr Gly Gln Val Leu Gly Ser Leu Val His Val
 35 40 45

aag ggc gcc aat gcc ggg gtc caa acc ttc ctg gga att cca ttt gcc 192
 Lys Gly Ala Asn Ala Gly Val Gln Thr Phe Leu Gly Ile Pro Phe Ala
 50 55 60

aag cca cct cta ggt ccg ctg cga ttt gca ccc cct gag ccc cct gaa 240
 Lys Pro Pro Leu Gly Pro Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
 65 70 75 80

tct tgg agt ggt gtg agg gat gga acc acc cat ccg gcc atg tgt cta 288
 Ser Trp Ser Gly Val Arg Asp Gly Thr Thr His Pro Ala Met Cys Leu
 85 90 95

cag gac ctc acc gca gtg gag tca gag ttt ctt agc cag ttc aac atg 336
 Gln Asp Leu Thr Ala Val Glu Ser Glu Phe Leu Ser Gln Phe Asn Met
 100 105 110

acc ttc cct tcc gac tcc atg tct gag gac tgc ctg tac ctc agc atc 384
 Thr Phe Pro Ser Asp Ser Met Ser Glu Asp Cys Leu Tyr Leu Ser Ile
 115 120 125

tac acg ccg gcc cat agc cat gaa ggc tct aac ctg ccg gtg atg gtg 432
 Tyr Thr Pro Ala His Ser His Glu Gly Ser Asn Leu Pro Val Met Val
 130 135 140

tgg atc cac ggt ggt gcg ctt gtt ttt ggc atg gct tcc ttg tat gat 480
 Trp Ile His Gly Gly Ala Leu Val Phe Gly Met Ala Ser Leu Tyr Asp
 145 150 155 160

ggt tcc atg ctg gct gcc ttg gag aac gtg gtg gtg gtc atc atc cag 528
 Gly Ser Met Leu Ala Ala Leu Glu Asn Val Val Val Val Ile Ile Gln
 165 170 175

tac cgc ctg ggt gtc ctg ggc ttc ttc agc act gga gac aag cac gca 576
 Tyr Arg Leu Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Lys His Ala
 180 185 190

acc ggc aac tgg ggc tac ctg gac caa gtg gct gca cta cgc tgg gtc	624
Thr Gly Asn Trp Gly Tyr Leu Asp Gln Val Ala Ala Leu Arg Trp Val	
195 200 205	
cag cag aat atc gcc cac ttt gga ggc aac cct gac cgt gtc acc att	672
Gln Gln Asn Ile Ala His Phe Gly Gly Asn Pro Asp Arg Val Thr Ile	
210 215 220	
ttt ggc gag tct gcg ggt ggc acg agt gtg tct tcg ctt gtt gtg tcc	720
Phe Gly Glu Ser Ala Gly Gly Thr Ser Val Ser Ser Leu Val Val Ser	
225 230 235 240	
ccc ata tcc caa gga ctc ttc cac gga gcc atc atg gag agt ggc gtg	768
Pro Ile Ser Gln Gly Leu Phe His Gly Ala Ile Met Glu Ser Gly Val	
245 250 255	
gcc ctc ctg ccc ggc ctc att gcc agc tca gct gat gtc atc tcc acg	816
Ala Leu Leu Pro Gly Leu Ile Ala Ser Ser Ala Asp Val Ile Ser Thr	
260 265 270	
gtg gtg gcc aac ctg tct gcc tgt gac caa gtt gac tct gag gcc ctg	864
Val Val Ala Asn Leu Ser Ala Cys Asp Gln Val Asp Ser Glu Ala Leu	
275 280 285	
gtg ggc tgc ctg cgg ggc aag agt aaa gag gag att ctt gca att aac	912
Val Gly Cys Leu Arg Gly Lys Ser Lys Glu Glu Ile Leu Ala Ile Asn	
290 295 300	
aag cct ttc aag atg atc ccc gga gtg gtg gat ggg gtc ttc ctg ccc	960
Lys Pro Phe Lys Met Ile Pro Gly Val Val Asp Gly Val Phe Leu Pro	
305 310 315 320	
agg cac ccc cag gag ctg ctg gcc tct gcc gac ttt cag cct gtc cct	1008
Arg His Pro Gln Glu Leu Leu Ala Ser Ala Asp Phe Gln Pro Val Pro	
325 330 335	
agc att gtt ggt gtc aac aac aat gaa ttc ggc tgg ctc atc ccc aag	1056
Ser Ile Val Gly Val Asn Asn Asn Glu Phe Gly Trp Leu Ile Pro Lys	
340 345 350	
gtc atg agg atc tat gat acc cag aag gaa atg gac aga gag gcc tcc	1104
Val Met Arg Ile Tyr Asp Thr Gln Lys Glu Met Asp Arg Glu Ala Ser	
355 360 365	
cag gct gct ctg cag aaa atg tta acg ctg ctg atg ttg cct cct aca	1152
Gln Ala Ala Leu Gln Lys Met Leu Thr Leu Leu Met Leu Pro Pro Thr	
370 375 380	
ttt ggt gac ctg ctg agg gag gag tac att ggg gac aat ggg gat ccc	1200
Phe Gly Asp Leu Leu Arg Glu Glu Tyr Ile Gly Asp Asn Gly Asp Pro	
385 390 395 400	
cag acc ctc caa gcg cag ttc cag gag atg atg gcg gac tcc atg ttt	1248
Gln Thr Leu Gln Ala Gln Phe Gln Glu Met Met Ala Asp Ser Met Phe	
405 410 415	

gtg atc cct gca ctc caa gta gca cat ttt cag tgt tcc cgg gcc cct	1296
Val Ile Pro Ala Leu Gln Val Ala His Phe Gln Cys Ser Arg Ala Pro	
420 425 430	
gtg tac ttc tac gag ttc cag cat cag ccc agc tgg ctc aag aac atc	1344
Val Tyr Phe Tyr Glu Phe Gln His Gln Pro Ser Trp Leu Lys Asn Ile	
435 440 445	
agg cca ccg cac atg aag gca gac cat ggt gat gag ctt cct ttt gtt	1392
Arg Pro Pro His Met Lys Ala Asp His Gly Asp Glu Leu Pro Phe Val	
450 455 460	
ttc aga agt ttc ttt ggg ggc aac tac att aaa ttc act gag gaa gag	1440
Phe Arg Ser Phe Phe Gly Gly Asn Tyr Ile Lys Phe Thr Glu Glu Glu	
465 470 475 480	
gag cag cta agc agg aag atg atg aag tac tgg gcc aac ttt gcg aga	1488
Glu Gln Leu Ser Arg Lys Met Met Lys Tyr Trp Ala Asn Phe Ala Arg	
485 490 495	
aat ggg aac ccc aat ggc gag ggt ctg cca cac tgg ccg ctg ttc gac	1536
Asn Gly Asn Pro Asn Gly Glu Gly Leu Pro His Trp Pro Leu Phe Asp	
500 505 510	
cag gag gag caa tac ctg cag ctg aac cta cag cct gcg gtg ggc cgg	1584
Gln Glu Glu Gln Tyr Leu Gln Leu Asn Leu Gln Pro Ala Val Gly Arg	
515 520 525	
gct ctg aag gcc cac agg ctc cag ttc tgg aag aag gcg ctg ccc caa	1632
Ala Leu Lys Ala His Arg Leu Gln Phe Trp Lys Lys Ala Leu Pro Gln	
530 535 540	
aag atc cag gag ctc gag gag cct gaa gag aga cac aca gag ctg tag	1680
Lys Ile Gln Glu Leu Glu Glu Pro Glu Glu Arg His Thr Glu Leu	
545 550 555	

<210> 7

<211> 559

<212> PRT

<213> Homo sapiens

<400> 7

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Ile Arg Thr Thr His Thr Gly Gln Val Leu Gly Ser Leu Val His Val	
35 40 45	
Lys Gly Ala Asn Ala Gly Val Gln Thr Phe Leu Gly Ile Pro Phe Ala	
50 55 60	
Lys Pro Pro Leu Gly Pro Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu	
65 70 75 80	

Ser	Trp	Ser	Gly	Val	Arg	Asp	Gly	Thr	Thr	His	Pro	Ala	Met	Cys	Leu	85	90	95
Gln	Asp	Leu	Thr	Ala	Val	Glu	Ser	Glu	Phe	Leu	Ser	Gln	Phe	Asn	Met	100	105	110
Thr	Phe	Pro	Ser	Asp	Ser	Met	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Ser	Ile	115	120	125
Tyr	Thr	Pro	Ala	His	Ser	His	Glu	Gly	Ser	Asn	Leu	Pro	Val	Met	Val	130	135	140
Trp	Ile	His	Gly	Gly	Ala	Leu	Val	Phe	Gly	Met	Ala	Ser	Leu	Tyr	Asp	145	150	155
Gly	Ser	Met	Leu	Ala	Ala	Leu	Glu	Asn	Val	Val	Val	Val	Ile	Ile	Gln	165	170	175
Tyr	Arg	Leu	Gly	Val	Leu	Gly	Phe	Phe	Ser	Thr	Gly	Asp	Lys	His	Ala	180	185	190
Thr	Gly	Asn	Trp	Gly	Tyr	Leu	Asp	Gln	Val	Ala	Ala	Leu	Arg	Trp	Val	195	200	205
Gln	Gln	Asn	Ile	Ala	His	Phe	Gly	Gly	Asn	Pro	Asp	Arg	Val	Thr	Ile	210	215	220
Phe	Gly	Glu	Ser	Ala	Gly	Gly	Thr	Ser	Val	Ser	Ser	Leu	Val	Val	Ser	225	230	235
Pro	Ile	Ser	Gln	Gly	Leu	Phe	His	Gly	Ala	Ile	Met	Glu	Ser	Gly	Val	245	250	255
Ala	Leu	Leu	Pro	Gly	Leu	Ile	Ala	Ser	Ser	Ala	Asp	Val	Ile	Ser	Thr	260	265	270
Val	Val	Ala	Asn	Leu	Ser	Ala	Cys	Asp	Gln	Val	Asp	Ser	Glu	Ala	Leu	275	280	285
Val	Gly	Cys	Leu	Arg	Gly	Lys	Ser	Lys	Glu	Glu	Ile	Leu	Ala	Ile	Asn	290	295	300
Lys	Pro	Phe	Lys	Met	Ile	Pro	Gly	Val	Val	Asp	Gly	Val	Phe	Leu	Pro	305	310	315
Arg	His	Pro	Gln	Glu	Leu	Leu	Ala	Ser	Ala	Asp	Phe	Gln	Pro	Val	Pro	325	330	335
Ser	Ile	Val	Gly	Val	Asn	Asn	Asn	Glu	Phe	Gly	Trp	Leu	Ile	Pro	Lys	340	345	350
Val	Met	Arg	Ile	Tyr	Asp	Thr	Gln	Lys	Glu	Met	Asp	Arg	Glu	Ala	Ser	355	360	365
Gln	Ala	Ala	Leu	Gln	Lys	Met	Leu	Thr	Leu	Leu	Met	Leu	Pro	Pro	Thr	370	375	380

Phe Gly Asp Leu Leu Arg Glu Glu Tyr Ile Gly Asp Asn Gly Asp Pro
385 390 395 400

Gln Thr Leu Gln Ala Gln Phe Gln Glu Met Met Ala Asp Ser Met Phe
405 410 415

Val Ile Pro Ala Leu Gln Val Ala His Phe Gln Cys Ser Arg Ala Pro
420 425 430

Val Tyr Phe Tyr Glu Phe Gln His Gln Pro Ser Trp Leu Lys Asn Ile
435 440 445

Arg Pro Pro His Met Lys Ala Asp His Gly Asp Glu Leu Pro Phe Val
450 455 460

Phe Arg Ser Phe Phe Gly Gly Asn Tyr Ile Lys Phe Thr Glu Glu Glu
465 470 475 480

Glu Gln Leu Ser Arg Lys Met Met Lys Tyr Trp Ala Asn Phe Ala Arg
485 490 495

Asn Gly Asn Pro Asn Gly Glu Gly Leu Pro His Trp Pro Leu Phe Asp
500 505 510

Gln Glu Glu Gln Tyr Leu Gln Leu Asn Leu Gln Pro Ala Val Gly Arg
515 520 525

Ala Leu Lys Ala His Arg Leu Gln Phe Trp Lys Lys Ala Leu Pro Gln
530 535 540

Lys Ile Gln Glu Leu Glu Glu Pro Glu Glu Arg His Thr Glu Leu
545 550 555

<210> 8

<211> 166

<212> PRT

<213> Homo sapiens

<400> 8

Trp Cys Gly Ser Thr Val Val Arg Leu Phe Leu Ala Trp Leu Pro Cys
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Met Met Val Pro Cys Trp Leu Pro Trp Arg Thr Trp Trp Trp Ser Ser
20 25 30

Ser Ser Thr Ala Trp Val Ser Trp Ala Ser Ser Ala Leu Glu Thr Ser
35 40 45

Thr Gln Pro Ala Thr Gly Ala Thr Trp Thr Lys Trp Leu His Tyr Ala
50 55 60

Gly Ser Ser Arg Ile Ser Pro Thr Leu Glu Ala Thr Leu Thr Val Ser
65 70 75 80

Pro Phe Leu Ala Ser Leu Arg Val Ala Arg Val Cys Leu Arg Leu Leu
85 90 95

Leu Thr Ser Leu Ser Arg
165